

Claims

1. Method for modifying the growth characteristics of a plant relative to corresponding wild type plants, comprising modifying expression in a plant of a seedy1 nucleic acid and/or modifying the level and/or activity in a plant of a seedy1 protein.
2. Method according to claim 1, wherein said modified expression and/or activity and/or level may be effected by introducing a genetic modification in the locus of a seedy1 gene.
3. Method according to claim 2, wherein said genetic modification is effected by any one or more of: TDNA activation, tilling, site-directed mutagenesis, homologous recombination or by introducing and expressing in a plant a seedy1 nucleic acid/gene or a portion thereof, or sequences capable of hybridising with the seedy1 nucleic acid/gene, which nucleic acid encodes a seedy1 protein or a homologue, derivative or active fragment thereof.
4. Method according to claim 2 or 3, wherein said seedy1 nucleic acid/gene or portion thereof, or sequence capable of hybridising with said seedy1 nucleic acid/gene, is over-expressed in a plant.
5. Method according to any one of claims 1 to 4, wherein said seedy1 nucleic acid is of plant origin, preferably from a dicotyledonous plant, further preferably from the family *Solanaceae*, more preferably from *Nicotiana*.
6. Method according to any one of claims 1 to 5, wherein said seedy1 nucleic acid is operably linked to a seed-preferred promoter.
7. Method according to claim 6, wherein said seed-preferred promoter is a prolamin promoter.
8. Method according to any one of claims 1 to 7, wherein said modified growth characteristic is selected from any one or more of: increased yield, increased biomass and modified plant architecture, each relative to corresponding wild type plants.
9. Method according to claim 8, wherein said increased yield is increased seed yield.
10. Method according to claim 8, wherein said modified architecture comprises increased biomass and increased number of panicles.

11. Plant or plant cell obtainable by a method according to any one of claims 1 to 10.
12. A genetic construct comprising:
- 5 (i) A seedy1 nucleic acid encoding a seedy1 protein;
- (ii) one or more control sequences capable of regulating expression of the nucleic acid of (i); and optionally
- (iii) a transcription termination sequence.
- 10 13. Construct according to claim 12, wherein said control sequence is a promoter, preferably a seed-preferred promoter.
14. Plant or plant cell transformed with a construct according to claim 12 or 13.
- 15 15. Method for the production of a transgenic plant having modified growth characteristics, which method comprises:
- (i) introducing into a plant or plant part a seedy1 nucleic acid encoding a seedy1 protein;
- (ii) cultivating the plant cell under conditions promoting regeneration and mature plant growth.
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16. Transgenic plant or plant cell having modified growth characteristics relative to corresponding wild type plants or plant cells, which modified growth characteristics result from a seedy1 nucleic acid introduced into said plant or plant cell.
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17. Transgenic plant or plant cell according to any one of claims 11, 14 or 16, wherein said plant is a monocotyledonous plant such as sugar cane, or wherein the plant is a crop plant such as soybean, sunflower, canola, alfalfa, rapeseed, cotton, tomato, potato or tobacco, or wherein the plant is a cereal, such as rice, maize, wheat, barley, millet, rye,
- 30 sorghum or oats.
18. Harvestable parts of a plant according to any one of claims 11, 14, 16 and 17, wherein said harvestable parts are preferably seeds.

19. Use of an isolated seedy1 nucleic acid and/or a seedy1 protein in modifying the growth characteristics of a plant, which growth characteristics are selected from any one or more of increased yield, increased biomass and modified plant architecture.

5 20. Use of an isolated seedy1 nucleic acid and/or a seedy1 protein in plant breeding.

21. An isolated seedy1 protein, comprising in the following order from N-terminus to C-terminus:

- 10 (i) a motif having at least 80% sequence identity to the sequence represented by SEQ ID NO 15; and
- (ii) a motif having at least 80% sequence identity to the sequence represented by SEQ ID NO 16; and
- (iii) a motif having at least 80% sequence identity to the sequence represented by SEQ ID NO 17 and which motif is a coiled coil motif; and
- 15 (iv) a motif having at least 80% sequence identity to the sequence represented by SEQ ID NO 18,

with the proviso that the seedy1 protein is not the *Arabidopsis* protein as deposited in Genbank under NCBI accession number AL161572 (SEQ ID NO 12).

20 22. An isolated seedy1 protein according to claim 21, wherein the motif according to SEQ ID NO: 15 is as represented by: (P/X)X((V/L/H)(Q/H)(V/I)W(N/X)NA(A/P)(F/C)D, wherein X may be any amino acid, and wherein

(P/X) preferably is P or is A or T or Q or another amino acid

(V/L/H) preferably is V or L or H

25 (Q/H) is either Q or H

(V/I) is either V or is T or S or another amino acid

(A/P) is preferably A or is P

(F/C) is preferably F or is C.

30 23. An isolated seedy1 protein according to claim 21, wherein the motif according to SEQ ID NO 17 is as represented by: (I/V/A)(D/E)XE(I/M)XX(I/V)(E/Q)XE(I/X)XRL(S/X)(S/X)(R/K) LXXLR(L/V/T/I)X(K/Q), where X may be any amino acid, and wherein:

(I/V/A) preferably is I or V or is A

(D/E) is either D or E

35 (I/M) preferably is I or is M

(I/V) preferably is I or is V

(E/Q) preferably is E or is Q

(I/X) preferably is I or is M or is V or any other amino acid

(S/X) preferably S or is T or any other amino acid

(S/X) preferably is S or is T or L or I or A

(R/K) preferably is R or is K

5 (L/V/T/I) preferably is L or T or V or I

(K/Q) preferably is K or Q

and which motif is a coiled coil motif.

10 24. An isolated seedy1 protein according to claim 21, wherein said motif according to SEQ ID NO 18 is as represented by: LP(R/K)I(R/X)(T/I)(M/X)(P/R)XX(D/X)(E/G)(S/T)(P/L)RDSG (C/X)(A/X)KR(V/X)(A/I)(D/E)(L/R)(V/X)(G/A)K, where X may be any amino acid, and wherein

(R/K) is either R or K

(R/X) is preferably R or is S or K

15 (T/I) is preferably T or I

(M/X) is preferably M or L or A or V

(P/R) is either P or R

(D/X) is preferably D or is G or T or N

(E/G) is preferably E or is G

20 (S/T) is preferably S or is T

(P/L) is preferably P or is L

(C/X) is preferably C or is P or A

(A/X) is preferably A or is V or I

(A/I) is preferably A or is I

25 (D/E) is either D or E

(L/R) is preferably L or is R

(V/X) is preferably V or is Q or N or I

(G/A) is preferably G or is A.

30 25. An isolated seedy1 nucleic acid/gene selected from:

(i) a nucleic acid represented by any one of SEQ ID NO: 1, 5 or 7 or the complement of any of the aforementioned;

(ii) a nucleic acid encoding an amino acid sequence represented by SEQ ID NO: 2, 4, 6, 8 or 10;

35 (iii) a nucleic acid encoding a homologue, derivative or active fragment of (i) or (ii) above;

(iv) a nucleic acid capable of hybridising with a nucleic acid of (i), (ii) or (iii) above;

- (v) a nucleic acid which is degenerate as a result of the genetic code from any one of the nucleic acids of (i) to (iv) above;
- (vi) a nucleic acid which is an allelic variant of any one of the nucleic acids of (i) to (v) above;
- 5 (vii) a nucleic acid which is an alternative splice variant of any one of the nucleic acids of (i) to (vi);
- (viii) a nucleic acid encoding a protein which has in increasing order of preference at least 21%, 22%, 23%, 24%, 25%, 26%, 27%, 28%, 29%, 30%, 31%, 32%, 33%, 34%, 35%, 36%, 37%, 38%, 39%, 40%, 41%, 42%, 43%, 44%, 45%, 46%, 10 47%, 48%, 49%, 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% sequence identity to any one or more from the sequences defined in (i) to (vii) above;
- (ix) a portion of a nucleic acid according to any of (i) to (viii) above;

15 wherein the nucleic acids of (i) to (ix) above encode a *seedy1* protein, and with the proviso that the isolated nucleic acid is not a rice cDNA as deposited under Genbank accession number AK063941 (SEQ ID NO 3), a *Medicago* BAC clone deposited as AC144618, AC139356, AC144482 or AC135566, the *Arabidopsis* cDNA deposited under AL61572 (SEQ ID NO 11) or the *Zea mays* EST deposited under AY108162 (SEQ ID NO 9).

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